What is claimed is:

1. A method for identifying a subject at risk of breast cancer, which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the one or more polymorphic variations are detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c);

whereby the presence of the polymorphic variation is indicative of the subject being at risk of breast cancer.

2. The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 185, 237, 641, 719, 990, 2908, 3140, 3880, 4494, 5107, 5220, 6031, 8670, 13794, 16356, 17164, 17264, 20537, 20637, 20900, 21155, 21795, 21931, 22167, 22656, 23108, 23404, 24287, 24480, 24592, 24878, 26370, 27056, 27874, 31248, 31458, 31553, 31637, 31668, 31752, 37643, 43941, 44134, 44329, 44343, 44362, 44818, 44917, 45215, 45666, 45680, 46402 ,46510, 46554 ,46823, 47714, 48963, 49157, 49254, 49257, 49356, 55202, 55527, 55916, 56402, 56413, 56685, 56783, 58044, ,58301 ,58382, 58393, 58869, 59155, 59189, 62546, 62568, 70983, 71465, 71538, 72144, 72340, 72527, 72968, 73397, 73553, 73720, 74190, 74687, 74699, 75580, 76345, 76506, 77554, 77889, 77919, 78866, 79061, 83777, 84360, 84631, 85775, 87153, 89650, 89895, 90103, 90234, 90309, 90376, 90925, 91561, 91605, 92954 and 94228.

4. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 185, 20537, 44329, 44362, 45666, 45680, 46510, 49254, 49356, 56402, 58301, 71465, 72527, 73553, 76345 and 83777.

5. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 18-8377 in SEQ ID NO: 1.

6. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 184, 506, 3981, 7815, 7875, 10775, 10786, 11013, 11020, 11101, 14171, 14278, 16512, 16706, 18442, 20286, 21591, 22275, 25318, 27997, 29840,31088, 31258, 32367, 32427, 33671, 38796, 41530, 41874, 44161, 47502, 51089, 51205, 53645, 54280, 57610, 57740, 60812, 60837, 64448, 65249, 65482, 66535, 66789, 67214, 68347, 69060, 70100, 70215, 73687, 73732, 74183, 74813, 78136, 79540, 79655, 79731, 82111, 82155, 83479, 84511, 85290, 90620, 91127, 92095, 92679, 94839 and 95220.

7. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 506, 3981, 7815, 7875, 11020, 11101, 18442, 47502, 53645, 65249, 73687, 73732, 74183, 79540, 82155, 85290, 90620, 91127, 92095, 92679, 94839 and 95220.

8. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 506-95220 in SEQ ID NO: 2.

9. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 186, 1332, 1893, 2786, 2962, 3377, 5522, 5621, 5889, 7531, 8268, 8923, 8988, 9117, 9448, 9494, 9628, 9640, 11072, 11150, 11379, 11692, 12056, 12104, 14160, 14836, 14980, 15165, 15315, 15624, 15796, 15939, 16581, 17045, 18501, 21800, 21966, 22134, 22181, 23028, 23312, 23573, 23858, 23888, 23990, 24073, 25330, 26473, 27958, 28421, 28804, 29322, 30819, 31956, 32592, 32818, 32880, 33244, 33845, 34272, 34931, 36870, 37790, 38708, 39135, 39919, 40166, 40985, 41049, 41935, 42775, 43807, 44254, 44814, 45249, 47599, 47807, 48555, 49249, 49293, 57566, 63587, 64560, 65432, 66291, 71331, 73344, 74159, 74564, 78194, 79128, 79393, 81579, 82574, 85309, 87076, 87844 and 90241.

10. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 5621, 9628, 9640, 21800, 21966, 22134, 22181, 23028, 23573, 23888, 24073, 26473, 27958, 28421, 28804, 29322, 30819, 31956, 32592, 32818, 32880, 33244, 33845, 34931, 37790, 38708, 39135, 39919, 40166, 41049, 43807, 44254, 45249, 47807, 48555, 49249, 49293, 57566, 63587, 64560, 65432, 66291, 71331, 73344, 74159, 78194, 79128, 81579 and 82574.

11. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 5621-82574 in SEQ ID NO: 3.

12. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 142, 693, 731, 879, 1084, 2249, 2519, 4461, 4616, 5109, 5270, 5436, 5457, 6536, 9665, 16120, 29489, 29524, 49159, 49273, 49596, 50135, 50184, 50393, 50401, 55750, 73843, 73852, 74052, 75382, 75662, 75942, 77917, 78821, 94813 and 97149.

13. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 16120 and 55750.

14. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 16120-55750 in SEQ ID NO: 4.

15. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 200, 381, 5303, 6084, 6879, 7837, 7985, 9333, 11559, 12473, 12880, 13606, 14861, 20658, 22200, 24525, 26373, 42869, 43713, 44429, 49037, 49170, 50206, 51552, 51674, 56427, 56844, 57953, 60862, 61606, 62560, 65078, 65155, 70295, 70335, 70398, 79233, 80025, 84521, 84540, 85170, 85300, 87596, 89696, 92219 and 96589.

16. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 12473, 20658, 24525, 49037, 49170, 51552, 51674, 70335, 84521, 87596, 92219 and 96589.

17. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 12473-96589 in SEQ ID NO: 5.

18. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in claim 3, 6, 9, 12 or 15.

19. The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

20. The method of claim 1, wherein the subject is a human.

21. A method for identifying a polymorphic variation associated with breast cancer proximal to an incident polymorphic variation associated with breast cancer, which comprises:

identifying a polymorphic variation proximal to the incident polymorphic variation associated with breast cancer, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation;

determining the presence or absence of an association of the proximal polymorphic variant with breast cancer.

22. The method of claim 18, wherein the incident polymorphic variation is at a position in claim 3, 6, 9, 12 or 15.

23. The method of claim 18, wherein the proximal polymorphic variation is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the incident polymorphic variation.

24. The method of claim 18, which further comprises determining whether the proximal polymorphic variation is in linkage disequilibrium with the incident polymorphic variation.

25. The method of claim 18, which further comprises identifying a second polymorphic variation proximal to the identified proximal polymorphic variation associated with breast cancer and determining if the second proximal polymorphic variation is associated with breast cancer.

26. The method of claim 22, wherein the second proximal polymorphic variant is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the proximal polymorphic variation associated with breast cancer.

27. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and

(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

wherein the nucleotide sequence comprises one or more polymorphic variants associated with breast cancer selected from the group consisting of a thymine at position 185 in SEQ ID NO: 1, a thymine at position 20537 in SEQ ID NO: 1, a cytosine at position 44329 in SEQ ID NO: 1, an adenine at position 44362 in SEQ ID NO: 1, a guanine at position 45666 in SEQ ID NO: 1, a thymine at position 45680 in SEQ ID NO: 1, a thymine at position 46510 in SEQ ID NO: 1, a guanine at position 49254 in SEQ ID NO: 1, a thymine at position 49356 in SEQ ID NO: 1, a guanine at position 56402 in SEQ ID NO: 1, a cytosine at position 58301 in SEQ ID NO: 1, an adenine at position 71465 in SEQ ID NO: 1, a guanine at position 72527 in SEQ ID NO: 1, a guanine at position 73553 in SEQ ID NO: 1, a thymine at position 76345 in SEQ ID NO: 1, an adenine at position 83777 in SEQ ID NO: 1, a cytosine at position 506 in SEQ ID NO: 2, a cytosine at position 3981 in SEQ ID NO: 2, a guanine at position 7815 in SEQ ID NO: 2, a guanine at position 7875 in SEQ ID NO: 2, a thymine at position 11020 in SEQ ID NO: 2, an adenine at position 11101 in SEQ ID NO: 2, an adenine at position 18442 in SEQ ID NO: 2, a cytosine at position 47502 in SEQ ID NO: 2, a guanine at position 53645 in SEQ ID NO: 2, a thymine at position 65249 in SEQ ID NO: 2, a cytosine at position 73687 in SEQ ID NO: 2, an adenine at position 73732 in SEQ ID NO: 2, a thymine at position 74183 in SEQ ID NO: 2, a thymine at position 79540 in SEQ ID NO: 2, a thymine at position 82155 in SEQ ID NO: 2, a cytosine at position 85290 in SEQ ID NO: 2, a guanine at position 90620 in SEQ ID NO: 2, a guanine at position 91127 in SEQ ID NO: 2, an adenine at position 92095 in SEQ ID NO: 2, a guanine at position 92679 in SEQ ID NO: 2, a guanine at position 94839 in SEQ ID NO: 2, a cytosine at position 95220 in SEQ ID NO: 2, a guanine at position 5621 in SEQ ID NO: 3, a guanine at position 9628 in SEQ ID NO: 3, a cytosine at position 9640 in SEQ ID NO:

3, a guanine at position 21800 in SEQ ID NO: 3, an adenine at position 21966 in SEQ ID NO: 3, a guanine at position 22134 in SEQ ID NO: 3, an adenine at position 22181 in SEQ ID NO: 3, a guanine at position 23028 in SEQ ID NO: 3, a thymine at position 23573 in SEQ ID NO: 3, a guanine at positino 23888 in SEQ ID NO: 3, an adenine at position 24073 in SEQ ID NO: 3, a thymine at position 26473 in SEQ ID NO: 3, a cytosine at position 27958 in SEQ ID NO: 3, an adenine at position 28421 in SEQ ID NO: 3, a thymine at position 28804 in SEQ ID NO: 3, a cytosine at position 29322 in SEQ ID NO: 3, a cytosine at position 30819 in SEQ ID NO: 3, a guanine at position 31956 in SEQ ID NO: 3, a guanine at position 32592 in SEQ ID NO: 3, a cytosine at position 32818 in SEQ ID NO: 3, a thymine at position 32880 in SEQ ID NO: 3, a cytosine at position 33244 in SEQ ID NO: 3, an adenine at position 33845 in SEQ ID NO: 3, a thymine at position 34931 in SEQ ID NO: 3, a thymine at position 37790 in SEQ ID NO: 3, a guanine at position 38708 in SEQ ID NO: 3, a thymine at position 39135 in SEQ ID NO: 3, an adenine at position 39919 in SEQ ID NO: 3, a thymine at position 40166 in SEQ ID NO: 3, a guanine at position 41049 in SEQ ID NO: 3, a cytosine at position 43807 in SEQ ID NO: 3, a guanine at position 44254 in SEQ ID NO: 3, a thymine at position 45249 in SEQ ID NO: 3, a guanine at position 47807 in SEQ ID NO: 3, a cytosine at position 48555 in SEQ ID NO: 3, an adenine at position 49249 in SEQ ID NO: 3, a cytosine at position 49293 in SEQ ID NO: 3, a cytosine at position 57566 in SEQ ID NO: 3, a cytosine at position 63587 in SEQ ID NO: 3, a thymine at position 64560 in SEQ ID NO: 3, a cytosine at position 65432 in SEQ ID NO: 3, a thymine at position 66291 in SEQ ID NO: 3, an adenine at position 71331 in SEQ ID NO: 3, a thymine at position 73344 in SEQ ID NO: 3, a thymine at position 74159 in SEQ ID NO: 3, an adenine at position 78194 in SEQ ID NO: 3, a cytosine at position 79128 in SEQ ID NO: 3, an adenine at position 81579 in SEQ ID NO: 3, a cytosine at position 82574 in SEQ ID NO: 3, a thymine at position 16120 in SEQ ID NO: 4, a cytosine at position 55750 in SEQ ID NO: 4, a cytosine at position 12473 in SEQ ID NO: 5, a thymine at position 20658 in SEQ ID NO: 5, a cytosine at position 24525 in SEQ ID NO: 5, a guanine at position 49037 in SEQ ID NO: 5, an adenine at position 49170 in SEQ ID NO: 5, a thymine at position 51552 in SEQ ID NO: 5, a guanine at position 51674 in SEQ ID NO: 5, a thymine at position 70335 in SEQ ID NO: 5, a guanine at position 84521 in SEQ ID NO: 5, an adenine at position 87596 in SEQ ID NO: 5, an adenine at position 92219 in SEQ ID NO: 5 and a thymine at position 96589 in SEQ ID NO: 5.

28. An oligonucleotide comprising a nucleotide sequence complementary to a portion of the nucleotide sequence of (a), (b), (c), or (d) in claim 24, wherein the 3' end of the oligonucleotide is adjacent to a polymorphic variation associated with breast cancer.

29. A microarray comprising an isolated nucleic acid of claim 24 linked to a solid support.

30. An isolated polypeptide encoded by the isolated nucleic acid sequence of claim 24.

31. A method for identifying a candidate molecule that modulates cell proliferation, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence in SEQ ID NO: 1-5;

(ii) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iv) a fragment of a nucleotide sequence of (i), (ii), or (iii); or

introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein,

whereby the presence of an interaction between the test molecule and the nucleic acid or protein identifies the test molecule as a candidate molecule that modulates cell proliferation.

32. The method of claim 28, wherein the system is an animal.

33. The method of claim 28, wherein the system is a cell.

34. The method of claim 28, wherein the nucleotide sequence comprises one or more polymorphic variations associated with breast cancer.

35. The method of claim 28, wherein the one or more polymorphic variations associated with breast cancer are at one or more positions in claim 3, 6, 9, 12 or 15.

36. A method for treating breast cancer in a subject, which comprises administering a candidate molecule identified by the method of claim 28 to a subject in need thereof, whereby the candidate molecule treats breast cancer in the subject.

37. A method for identifying a candidate therapeutic for treating breast cancer, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence in SEQ ID NO: 1-5;

(ii) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iv) a fragment of a nucleotide sequence of (i), (ii), or (iii); or

introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein,

whereby the presence of an interaction between the test molecule and the nucleic acid or protein identifies the test molecule as a candidate therapeutic for treating breast cancer.

38. The method of claim 34, wherein the test molecule inhibits cell proliferation or cell metastasis.

39. A method for treating breast cancer in a subject, which comprises contacting one or more cells of a subject in need thereof with a nucleic acid, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and

(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

whereby contacting the one or more cells of the subject with the nucleic acid treats breast cancer in the subject.

40. The method of claim 36, wherein the nucleic acid is RNA or PNA.

41. The method of claim 37, wherein the nucleic acid is duplex RNA.

42. A method for treating breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the one or more polymorphic variation are detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

administering a breast cancer treatment to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

43. The method of claim 39, wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

44. The method of claim 39, wherein the breast cancer treatment comprises a nucleic acid comprising a nucleotide sequence complementary to a nucleotide sequence in SEQ ID NO: 1-5.

45. The method of claim 41, wherein the nucleic acid is a double stranded RNA.

46. The method of claim 39, which further comprises extracting and analyzing a tissue biopsy sample from the subject.

47. The method of claim 43, wherein the treatment is chemotherapy, surgery, radiation therapy, and combinations of the foregoing.

48. The method of claim 44, wherein the chemotherapy is selected from the group consisting of cyclophosphamide (Cytoxan), methotrexate (Amethopterin, Mexate, Folex), fluorouracil (Fluorouracil, 5-Fu, Adrucil), cyclophosphamide, doxorubicin (Adriamycin), and combinations of the foregoing.

49. The method of claim 45, wherein the combinations are selected from the group consisting of cyclophosphamide (Cytoxan), methotrexate (Amethopterin, Mexate, Folex), and fluorouracil (Fluorouracil, 5-Fu, Adrucil); cyclophosphamide, doxorubicin (Adriamycin), and fluorouracil; and doxorubicin and cyclophosphamide.

50. The method of claim 39, wherein the breast cancer treatment reduces breast cancer metastasis.

51. A method for detecting or preventing breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

administering a breast cancer prevention procedure or detection procedure to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

52. The method of claim 48, wherein the one or more polymorphic variations are detected at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

53. The method of claim 48, wherein the breast cancer detection procedure is selected from the group consisting of a mammography, an early mammography program, a frequent mammography program, a biopsy procedure, a breast biopsy and biopsy from another tissue, a breast ultrasound and optionally ultrasound analysis of another tissue, breast magnetic resonance imaging (MRI) and optionally MRI analysis of another tissue, electrical impedance (T-scan) analysis of breast and optionally of another tissue, ductal lavage, nuclear medicine analysis (e.g., scintimammography), *BRCA1* and/or *BRCA2* sequence analysis results, thermal imaging of the breast and optionally of another tissue, and a combination of the foregoing.

54. The method of claim 48, wherein the breast cancer prevention procedure is selected from the group consisting of one or more selective hormone receptor modulators, one or more compositions that prevent production of hormones, one or more hormonal treatments, one or more biologic response modifiers, surgery, and drugs that delay or halt metastasis.

55. The method of claim 51, wherein the selective hormone receptor modulator is selected from the group consisting of tamoxifen, reloxifene, and toremifene; the composition that prevents production of hormones is an aramotase inhibitor selected from the group consisting of exemestane, letrozole, anastrozol, groserelin, and megestrol; the hormonal treatment is selected from the group consisting of goserelin acetate and fulvestrant; the biologic response modifier is an antibody that specifically binds herceptin/HER2; the surgery is selected from the group consisting of lumpectomy and mastectomy; and the drug that delays or halts metastasis is pamidronate disodium.

56. A method of targeting information for preventing or treating breast cancer to a subject in need thereof, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

directing information for preventing or treating breast cancer to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

57. The method of claim 53, wherein the one or more polymorphic variations are detected at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

58. The method of claim 53, wherein the information comprises a description of a breast cancer detection procedure, a chemotherapeutic treatment, a surgical treatment, a radiation treatment, a preventative treatment of breast cancer, and combinations of the foregoing.

59. A method of selecting a subject that will respond to a treatment of breast cancer, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide consisting of an amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5 ;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to an amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5 ; and

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

selecting a subject that will respond to the breast cancer treatment based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

60. The method of claim 56, wherein the one or more polymorphic variations are at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

61. A composition comprising a breast cancer cell and an antibody that specifically binds to a protein, polypeptide or peptide encoded by a nucleotide sequence identical to or 90% or more identical to a nucleotide sequence in SEQ ID NO: 1-11.

62. The composition of claim 58, wherein the antibody specifically binds to an epitope that comprises a lysine at amino acid position 237 of SEQ ID NO: 12, a proline at amino acid position 413 of SEQ ID NO: 16 or a glutamine at amino acid position 63 of SEQ ID NO: 16.

63. A composition comprising a breast cancer cell and a RNA, DNA, PNA or ribozyme molecule comprising a nucleotide sequence identical to or 90% or more identical to a portion of a nucleotide sequence in SEQ ID NO: 1-11.

64. The composition of claim 60, wherein the RNA molecule is a short inhibitory RNA molecule.